

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	17	f0f1 adj atpase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 14:03
L2	11	f0f1-atpase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 14:03
L3	123	H+-atpase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 14:03
L4	214	H+ adj atpase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 14:03
L5	230	L1 or L2 or L3 or L4	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 14:03
L6	6	L5 and (tomita.in. or yokota.in.)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 14:03
S1	33711	method and biotinylat\$	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 11:06
S2	899	(method and biotinylat\$).clm.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 11:10
S3	17	S2 and biotinylat\$.ti.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 12:40
S4	17	f0f1 adj atpase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 12:41
S5	11	f0f1-atpase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 12:41

EAST Search History

S6	123	H+-atpase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 12:41
S7	214	H+ adj atpase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 12:41
S8	230	S4 or S5 or S6 or S7	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 14:03
S9	4	S8 and ammoniagenes	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 12:41
S10	31	S8 and (coryneform or corynebacterium)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 12:44
S11	47	S8 and subtilis	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 12:44
S12	17	f0f1 adj atpase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 13:17
S13	11	f0f1-atpase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 13:17
S14	123	H+-atpase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 13:17
S15	214	H+ adj atpase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 13:17
S16	230	S12 or S13 or S14 or S15	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/05/12 14:03



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#6 Search ammoniagenes	12:18:20	141
#4 Search #3 AND ammoniagenes	12:17:52	0
#3 Search "Proton-Translocating ATPases"[MeSH]	12:17:27	8670

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May 9 2006 14:13:00

IUBMB Enzyme Nomenclature

EC 3.6.3.14

Common name: H⁺-transporting two-sector ATPase

Reaction: ATP + H₂O + H⁺_{in} = ADP + phosphate + H⁺_{out}

Glossary: F_o the "o" refers to oligomycin. F₀ is incorrect.

Other names: ATP synthase; F₁-ATPase; F₀F₁-ATPase; H⁺-transporting ATPase; mitochondrial ATPase; coupling factors (F₀, F₁ and CF₁); chloroplast ATPase; bacterial Ca²⁺/Mg²⁺ ATPase

Systematic name: ATP phosphohydrolase (H⁺-transporting)

Comments: A multisubunit non-phosphorylated ATPase that is involved in the transport of ions. Large enzymes of mitochondria, chloroplasts and bacteria with a membrane sector (F_o, V_o, A_o) and a cytoplasmic-compartment sector (F₁, V₁, A₁). The F-type enzymes of the inner mitochondrial and thylakoid membranes act as ATP synthases. All of the enzymes included here operate in a rotational mode, where the extramembrane sector (containing 3 α- and 3 β-subunits) is connected via the δ-subunit to the membrane sector by several smaller subunits. Within this complex, the γ- and ε-subunits, as well as the 9-12 c subunits rotate by consecutive 120° angles and perform parts of ATP synthesis. This movement is driven by the H⁺ electrochemical potential gradient. The V-type (in vacuoles and clathrin-coated vesicles) and A-type (archebacterial) enzymes have a similar structure but, under physiological conditions, they pump H⁺ rather than synthesize ATP.

Links to other databases: [BRENDA](#), [EXPASY](#), [KEGG](#), [ERGO](#), [PDB](#), CAS registry number:

References:

1. Boyer, P.D. The binding change mechanism for ATP synthase - some probabilities and possibilities. *Biochim. Biophys. Acta* 1140 (1993) 215-250. [Medline UI: [93112640](#)]
2. Abrahams, J.P., Leslie, A.G.W., Lutter, R. and Walker, J.F. Structure at 2.8 Å resolution of F₁-ATPase from bovine heart mitochondria. *Nature* 375 (1994) 621-628. [Medline UI: [94344236](#)]
3. Blair, A., Ngo, L., Park, J., Paulsen, I.T. and Saier, M.H., Jr. Phylogenetic analyses of the homologous transmembrane channel-forming proteins of the F₀F₁-ATPases of bacteria, chloroplasts and mitochondria. *Microbiology* 142 (1996) 17-32. [Medline UI: [96146047](#)]
4. Noji, H., Yasuda, R., Yoshida, M. and Kinosita, K., Jr. Direct observation of the rotation of F₁-ATPase. *Nature* 386 (1997) 299-302. [Medline UI: [97222141](#)]

[EC 3.6.3.14 created 1984 as EC 3.6.1.34, transferred 2000 to EC 3.6.3.14]

Return to [EC 3.6.3 home page](#)

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Search Strategy for 10/694,779

(FILE 'HOME' ENTERED AT 14:04:27 ON 12 MAY 2006)

FILE 'REGISTRY' ENTERED AT 14:05:15 ON 12 MAY 2006

L1 9 S 3.6.3.14
 E "3.6.3.14"/CN 25
 E "ATPASE"/CN 25
L2 1 S E3

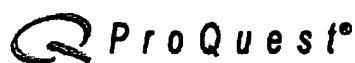
FILE 'MEDLINE, AGRICOLA, CAPLUS, BIOSIS, EMBASE, WPIDS' ENTERED AT
14:10:39 ON 12 MAY 2006

L3 3 S (L2 OR ATPASE) AND AMMONIAGENES
L4 2 DUP REM L3 (1 DUPLICATE REMOVED)

FILE 'CAPLUS' ENTERED AT 14:12:04 ON 12 MAY 2006

 E TOMITA F/AU 25
L5 252 S (E18)
 E YOKOTA A/AU 25
L6 157 S (E29)
L7 15 S (L5 OR L6) AND ATPASE
L8 15 DUP REM L7 (0 DUPLICATES REMOVED)
L9 15 S L8
L10 1 S L8 AND AMMONIAGENES

=>

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OM nucleic - nucleic search, using sw model

Run on: March 17, 2006, 10:56:35 ; Search time 45481 Seconds
 (without alignments)
 11873.371 Million cell updates/sec

Title: US-10-694-779-21
 Perfect score: 9500
 Sequence: 1 acctcgtatgggcagtaatt.....acgggcaacgcgtccgcggg 9500

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : GenEmbl:*
 1: gb_ba:*
 2: gb_in:*
 3: gb_env:*
 4: gb_om:*
 5: gb_ov:*
 6: gb_pat:*
 7: gb_ph:*
 8: gb_pr:*
 9: gb_ro:*
 10: gb_sts:*
 11: gb_sy:*
 12: gb_un:*
 13: gb_vi:*
 14: gb_htg:*
 15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	9500	100.0	9500	6	BD133267	BD133267 FOF1-ATPa
2	4259	44.8	110000	1	BA000035_13	Continuation (14 o
3	4229	44.5	349459	1	BX927151	BX927151 Corynebac
4	4227.4	44.5	110000	1	BA000036_12	Continuation (13 o
5	4227.4	44.5	349980	6	AX127147	AX127147 Sequence
6	4131.2	43.5	8394	1	AB046112	AB046112 Corynebac
7	4130	43.5	8001	1	AB048368	AB048368 Brevibact

	8	4060.4	42.7	347625	1	BX248356	BX248356 Corynebac
c	9	3723.8	39.2	110000	1	CR931997_15	Continuation (16 o
	10	2596.8	27.3	110000	1	AP006618_11	Continuation (12 o
c	11	1863.8	19.6	110000	1	CP000088_28	Continuation (29 o
c	12	1798.4	18.9	302325	1	AE017236	AE017236 Mycobacte
	13	1798.2	18.9	7760	1	AY702091	AY702091 Nonomurae
	14	1750.8	18.4	299450	1	BX248338	BX248338 Mycobacte
	15	1749.2	18.4	110000	1	AE000516_14	Continuation (15 o
	16	1749.2	18.4	348264	1	BX842576	BX842576 Mycobacte
	17	1735.2	18.3	110000	1	AE016822_06	Continuation (7 of
	18	1735.2	18.3	110000	1	AE016822_07	Continuation (8 of
c	19	1732.4	18.2	36241	1	MLU15186	U15186 Mycobacteri
c	20	1732.4	18.2	36241	6	AR345366	AR345366 Sequence
	21	1732.4	18.2	348450	1	MLEPRTN4	AL583920 Mycobacte
c	22	1667.2	17.5	110000	1	AE014295_12	Continuation (13 o
c	23	1667.2	17.5	349980	6	AX492782	AX492782 Sequence
c	24	1667.2	17.5	349980	6	AX553949	AX553949 Sequence
c	25	1665.2	17.5	110000	1	BA000030_35	Continuation (36 o
	26	1662.8	17.5	300100	1	SCO939123	AL939123 Streptomy
	27	1638	17.2	1638	6	BD133259	BD133259 FOF1-ATPa
	28	1618.8	17.0	8560	1	SLATPSYNA	Z22606 S.lividans
	29	1618.4	17.0	8358	1	AY488174	AY488174 Bifidobac
c	30	1606.4	16.9	110000	1	AE017283_13	Continuation (14 o
c	31	1474.2	15.5	8323	1	AY488175	AY488175 Bifidobac
c	32	1474.2	15.5	20798	6	CQ363832	CQ363832 Sequence
	33	1443	15.2	1443	6	BD133261	BD133261 FOF1-ATPa
	34	1170.8	12.3	1572	6	AX065635	AX065635 Sequence
	35	1159	12.2	1764	6	AX065633	AX065633 Sequence
	36	1158.6	12.2	1674	6	BD163541	BD163541 Novel pol
	37	1158.6	12.2	1674	6	AX121424	AX121424 Sequence
	38	1097.8	11.6	1452	6	E09634	E09634 Brevibacter
	39	1096.2	11.5	1452	1	CGASO19	X76875 C.glutamicu
	40	1092.6	11.5	1449	6	BD163543	BD163543 Novel pol
	41	1092.6	11.5	1449	6	AX121426	AX121426 Sequence
	42	1073	11.3	299050	1	BX251411	BX251411 Tropherym
c	43	1073	11.3	302529	1	AE016851	AE016851 Tropherym
	44	1054.4	11.1	110000	1	AP006840_01	Continuation (2 of
c	45	1039.8	10.9	349315	1	BX572593	BX572593 Rhodopseu

Me

181993

STIC-Biotech/ChemLib

From: Steadman, David (AU1652)
Sent: Monday, March 13, 2006 7:02 AM
To: STIC-Biotech/ChemLib
Subject: 10/694,779 sequence search request

NAME: David Steadman
AU: 1656
Date: 3/13/06
Office: Remsen 2B05
Mailbox: Remsen 3C70

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Please search the following sequence in commercial databases:

- 1) Standard search of SEQ ID NO:9 against nucleic acid databases.
- 2) Standard search of SEQ ID NO:21 against nucleic acid databases.

Please align the following sequences:

SEQ ID NO:9 against SEQ ID NO:21

Please save results to diskette.

Thank you very much.

David J. Steadman, Ph.D.
Primary Examiner
Art Unit 1656
Protein Crystallography and Recombinant Enzymes
Office: Remsen 2B05
Mailbox: Remsen 3C70
Phone: (571) 272-0942

Searcher: _____
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Date completed: _____
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NA# _____ AA# _____
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Structure #: _____ Text: _____
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Run on: March 17, 2006, 13:22:35 ; Search time 1018 Seconds
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Title: US-10-694-779-21
Perfect score: 9500
Sequence: 1 acctcgtatgggcagtaatt.....acgggcaacgcgtccgcggg 9500

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

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SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
c	1	1749.2	18.4	4403765	3 US-09-103-840A-2	Sequence 2, Appli
	2	1749.2	18.4	4411529	3 US-09-103-840A-1	Sequence 1, Appli
	3	1732.4	18.2	36241	3 US-08-311-731A-134	Sequence 134, App
	4	780.4	8.2	10399	3 US-08-961-527-160	Sequence 160, App
	5	758.6	8.0	4815	3 US-09-254-504-1	Sequence 1, Appli
c	6	605.2	6.4	1407	3 US-09-252-991A-2510	Sequence 2510, Ap
	7	605.2	6.4	1416	3 US-09-252-991A-2404	Sequence 2404, Ap
	8	555.2	5.8	1497	3 US-09-489-039A-3622	Sequence 3622, Ap

	9	553.6	5.8	72704	3	US-09-902-540-1273	Sequence 1273, Ap
	10	553	5.8	1446	3	US-09-902-540-5772	Sequence 5772, Ap
	11	549.4	5.8	1416	3	US-09-107-433-2281	Sequence 2281, Ap
	12	548	5.8	1407	3	US-09-583-110-725	Sequence 725, App
c	13	546.4	5.8	1830121	3	US-09-557-884-1	Sequence 1, Appli
c	14	546.4	5.8	1830121	3	US-09-643-990A-1	Sequence 1, Appli
c	15	546.4	5.8	1830121	3	US-10-158-865-1	Sequence 1, Appli
	16	516.2	5.4	1548	3	US-09-902-540-7415	Sequence 7415, Ap
	17	516.2	5.4	5245	3	US-09-902-540-714	Sequence 714, App
	18	515.2	5.4	6309	3	US-08-956-171E-480	Sequence 480, App
	19	515.2	5.4	6309	3	US-08-781-986A-480	Sequence 480, App
	20	515.2	5.4	94750	3	US-09-596-002-38	Sequence 38, Appl
	21	508.8	5.4	1883	3	US-09-949-016-576	Sequence 576, App
	22	508.8	5.4	1914	3	US-09-949-016-2016	Sequence 2016, Ap
	23	508.2	5.3	3014	3	US-09-710-279-3680	Sequence 3680, Ap
c	24	498.6	5.2	1812	3	US-09-533-559-2	Sequence 2, Appli
	25	493.4	5.2	1428	3	US-09-134-001C-1413	Sequence 1413, Ap
	26	491.8	5.2	1413	3	US-09-710-279-1813	Sequence 1813, Ap
	27	483.2	5.1	1410	3	US-09-543-681A-3361	Sequence 3361, Ap
	28	476.6	5.0	1434	3	US-09-107-532A-1705	Sequence 1705, Ap
	29	474.8	5.0	1434	3	US-09-134-000C-2498	Sequence 2498, Ap
	30	472.2	5.0	1807	3	US-09-377-497-4	Sequence 4, Appli
	31	458.8	4.8	1899	2	US-08-634-331-2	Sequence 2, Appli
	32	457.8	4.8	1557	3	US-09-252-991A-2591	Sequence 2591, Ap
c	33	457.8	4.8	1773	3	US-09-252-991A-2327	Sequence 2327, Ap
	34	456.6	4.8	1566	3	US-09-107-532A-3134	Sequence 3134, Ap
	35	447.6	4.7	1491	3	US-09-540-236-920	Sequence 920, App
	36	446.2	4.7	1410	3	US-09-328-352-696	Sequence 696, App
	37	445.4	4.7	1596	3	US-09-248-796A-3333	Sequence 3333, Ap
	38	437.8	4.6	1374	2	US-08-743-637B-187	Sequence 187, App
	39	431.6	4.5	1554	3	US-09-489-039A-3553	Sequence 3553, Ap
c	40	431.6	4.5	1737	3	US-09-489-039A-3428	Sequence 3428, Ap
	41	428.8	4.5	3080	3	US-09-710-279-3855	Sequence 3855, Ap
	42	427	4.5	1512	3	US-09-134-001C-1377	Sequence 1377, Ap
	43	427	4.5	1512	3	US-09-710-279-1809	Sequence 1809, Ap
	44	421	4.4	1506	3	US-09-583-110-723	Sequence 723, App
	45	421	4.4	1536	3	US-09-107-433-1185	Sequence 1185, Ap

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OM nucleic - nucleic search, using sw model

Run on: March 17, 2006, 19:49:10 ; Search time 1832 Seconds
(without alignments)
12091.269 Million cell updates/sec

Title: US-10-694-779-21
Perfect score: 9500
Sequence: 1 acctcgtatgggcagtaatt.....acgggcaacgcgtccgcggg 9500

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_New:*
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2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq1:*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	613.4	6.5	1457619	12 US-11-098-686-8739	Sequence 8739, Ap
2	508.8	5.4	1662	8 US-10-821-234-784	Sequence 784, App
3	508.2	5.3	3014	8 US-10-793-626-3680	Sequence 3680, Ap
4	494	5.2	1437	12 US-11-074-176-167	Sequence 167, App

	5	491.8	5.2	1413	8	US-10-793-626-1813	Sequence 1813, Ap
	6	485.6	5.1	1395	8	US-10-467-657-1291	Sequence 1291, Ap
	7	453.2	4.8	1638	7	US-10-932-182A-75392	Sequence 75392, A
	8	453.2	4.8	1638	7	US-10-932-182A-75392	Sequence 75392, A
	9	448.4	4.7	1929	12	US-11-119-351-9	Sequence 9, Appli
	10	447.2	4.7	1647	7	US-10-932-182A-2757	Sequence 2757, Ap
	11	447.2	4.7	1647	7	US-10-932-182A-2757	Sequence 2757, Ap
	12	445.2	4.7	1509	12	US-11-074-176-349	Sequence 349, App
	13	445.2	4.7	1518	12	US-11-074-176-175	Sequence 175, App
	14	438.2	4.6	1521	12	US-11-098-686-9301	Sequence 9301, Ap
	15	428.8	4.5	3080	8	US-10-793-626-3855	Sequence 3855, Ap
	16	427	4.5	1512	8	US-10-793-626-1809	Sequence 1809, Ap
	17	426.2	4.5	1536	7	US-10-932-182A-1477	Sequence 1477, Ap
	18	426.2	4.5	1536	7	US-10-932-182A-1477	Sequence 1477, Ap
	19	425.6	4.5	1416	12	US-11-098-686-9303	Sequence 9303, Ap
	20	420.6	4.4	1545	8	US-10-467-657-1287	Sequence 1287, Ap
	21	406.6	4.3	1536	7	US-10-932-182A-77398	Sequence 77398, A
	22	406.6	4.3	1536	7	US-10-932-182A-77398	Sequence 77398, A
	23	383.6	4.0	611587	12	US-11-117-187-209	Sequence 209, App
c	24	382.2	4.0	3599	8	US-10-793-626-4003	Sequence 4003, Ap
c	25	340.8	3.6	5669	7	US-10-527-048-13	Sequence 13, Appl
c	26	340.8	3.6	5834	7	US-10-527-048-15	Sequence 15, Appl
c	27	340.8	3.6	6465	7	US-10-527-048-25	Sequence 25, Appl
c	28	340.8	3.6	6659	7	US-10-527-048-22	Sequence 22, Appl
c	29	340.8	3.6	7057	7	US-10-527-048-26	Sequence 26, Appl
c	30	340.8	3.6	7510	7	US-10-527-048-19	Sequence 19, Appl
c	31	340.8	3.6	7549	7	US-10-527-048-24	Sequence 24, Appl
c	32	340.8	3.6	8327	7	US-10-527-048-23	Sequence 23, Appl
	33	337.6	3.6	1887	7	US-10-527-048-8	Sequence 8, Appli
c	34	337.2	3.5	1352	8	US-10-485-517-72	Sequence 72, Appl
	35	237.4	2.5	1066	12	US-11-136-527-4053	Sequence 4053, Ap
	36	225.6	2.4	902	12	US-11-128-061-217	Sequence 217, App
	37	225.6	2.4	902	12	US-11-128-049-217	Sequence 217, App
	38	211.4	2.2	600	12	US-11-128-061-3859	Sequence 3859, Ap
	39	211.4	2.2	600	12	US-11-128-049-3859	Sequence 3859, Ap
	40	208	2.2	517	6	US-09-925-065A-327316	Sequence 327316,
	41	208	2.2	517	6	US-09-925-065A-327317	Sequence 327317,
c	42	205	2.2	573	6	US-09-925-065A-611756	Sequence 611756,
c	43	204.6	2.2	573	6	US-09-925-065A-611757	Sequence 611757,
c	44	197.4	2.1	542	6	US-09-925-065A-327793	Sequence 327793,
c	45	195.8	2.1	542	6	US-09-925-065A-327794	Sequence 327794,

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2006, 05:44:57 ; Search time 1112 Seconds
 (without alignments)
 5466.007 Million cell updates/sec

Title: US-10-694-779-9
 Perfect score: 912
 Sequence: 1 atgtgcgacggagtcctag.....cacttcacgcagactcgcac 912

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_21:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	912	100.0	912	6	ABL54659	Abl54659 Corynebac
2	912	100.0	9500	6	ABL54671	Abl54671 Corynebac
3	504.2	55.3	349980	5	AAH68528	Aah68528 C glutami

	4	488.2	53.5	933	4	AAF71737	Aaf71737 Corynebac
	5	456.2	50.0	862	4	AAF71738	Aaf71738 Corynebac
	6	454	49.8	940	8	ACA29621	Aca29621 Prokaryot
	7	443.6	48.6	810	5	AAH66301	Aah66301 C glutami
c	8	118.8	13.0	349980	6	ABQ81844	Abq81844 Bifidobac
	9	50.8	5.6	843	14	ACL66536	Acl66536 M. xanthu
c	10	50.8	5.6	1394	14	ACL63902	Acl63902 M. xanthu
	11	48.8	5.4	4364	4	AAS59660	Aas59660 Propionib
	12	48.8	5.4	4364	8	ACF64589	Acf64589 Propionib
	13	48.4	5.3	543	13	ADS59769	Ads59769 Bacterial
	14	48.4	5.3	732	13	ADS62938	Ads62938 Bacterial
	15	48.4	5.3	732	13	ADS62291	Ads62291 Bacterial
	16	48.4	5.3	732	13	ADS62785	Ads62785 Bacterial
	17	48.4	5.3	849	8	ACA25438	Aca25438 Prokaryot
	18	47.2	5.2	849	8	ACA26013	Aca26013 Prokaryot
c	19	47.2	5.2	2000	8	ADA71938	Ada71938 Rice gene
	20	44.6	4.9	1703	4	AAD02475	Aad02475 cDNA clon
	21	43.8	4.8	2000	8	ADA71938	Ada71938 Rice gene
	22	43	4.7	879	8	ACA27392	Aca27392 Prokaryot
	23	40.2	4.4	849	8	ACA23312	Aca23312 Prokaryot
c	24	40	4.4	680	3	AAF08703	Aaf08703 Fusarium
c	25	40	4.4	680	13	ADU52744	Adu52744 Fusarium
c	26	40	4.4	680	14	ADZ90747	Adz90747 Fusarium
c	27	39	4.3	1581	3	AAA93691	Aaa93691 Agrobacte
c	28	39	4.3	1581	4	AAF86183	Aaf86183 Mannose i
c	29	39	4.3	1581	8	ACA61518	Aca61518 Modified
	30	38	4.2	693	8	ACA25636	Aca25636 Prokaryot
	31	37.8	4.1	702	14	ACL70731	Acl70731 M. xanthu
	32	37.8	4.1	726	13	ADT44413	Adt44413 Bacterial
c	33	37.8	4.1	6430	14	ACL64206	Acl64206 M. xanthu
	34	37	4.1	663	11	ACH94558	Ach94558 Klebsiell
	35	37	4.1	696	8	ACA25755	Aca25755 Prokaryot
	36	36.6	4.0	795	14	ADY77504	Ady77504 A. thalia
	37	36.6	4.0	1813	12	ADM47591	Adm47591 Polynucle
	38	36.6	4.0	1865	4	AAD02473	Aad02473 cDNA clon
c	39	36.6	4.0	35829	4	AAS59573	Aas59573 Propionib
c	40	36.6	4.0	35829	8	ACF64502	Acf64502 Propionib
	41	36.4	4.0	1256	13	ADX35007	Adx35007 Plant ful
	42	36.4	4.0	2145	9	ADA48625	Ada48625 Rice gene
	43	36.4	4.0	2145	11	ACL30288	Acl30288 Rice abio
	44	36.4	4.0	2187	8	ADA69492	Ada69492 Rice gene
	45	36.4	4.0	2189	9	ADA48499	Ada48499 Rice gene

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2006, 22:16:24 ; Search time 1455 Seconds
(without alignments)
5183.280 Million cell updates/sec

Title: US-10-694-779-9
Perfect score: 912
Sequence: 1 atgtgcgacggagtcgtag.....cacttcacgcagactcgcac 912

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	912	100.0	912	3	US-09-901-884-9	Sequence 9, Appli
2	912	100.0	912	8	US-10-694-779-9	Sequence 9, Appli
3	912	100.0	9500	3	US-09-901-884-21	Sequence 21, Appl
4	912	100.0	9500	8	US-10-694-779-21	Sequence 21, Appl
5	504.2	55.3	3309400	3	US-09-738-626-1	Sequence 1, Appli
6	488.2	53.5	933	8	US-10-781-014-755	Sequence 755, App
7	456.2	50.0	862	8	US-10-781-014-757	Sequence 757, App

	8	454	49.8	940	7	US-10-282-122A-17491	Sequence 17491, A
	9	443.6	48.6	810	3	US-09-738-626-1336	Sequence 1336, Ap
	10	119.4	13.1	807	6	US-10-156-761-2874	Sequence 2874, Ap
	11	119.4	13.1	125746	6	US-10-156-761-15102	Sequence 15102, A
c	12	119.4	13.1	9025608	6	US-10-156-761-1	Sequence 1, Appli
c	13	118.8	13.0	2256646	7	US-10-470-565-1	Sequence 1, Appli
	14	48.4	5.3	543	6	US-10-369-493-35443	Sequence 35443, A
	15	48.4	5.3	732	6	US-10-369-493-37965	Sequence 37965, A
	16	48.4	5.3	732	6	US-10-369-493-38459	Sequence 38459, A
	17	48.4	5.3	732	6	US-10-369-493-38612	Sequence 38612, A
	18	48.4	5.3	849	7	US-10-282-122A-13308	Sequence 13308, A
	19	47.2	5.2	849	7	US-10-282-122A-13883	Sequence 13883, A
	20	44.6	4.9	864	8	US-10-425-115-56270	Sequence 56270, A
	21	43	4.7	879	7	US-10-282-122A-15262	Sequence 15262, A
	22	42.6	4.7	1160	5	US-10-123-155-234	Sequence 234, App
	23	42.6	4.7	1160	6	US-10-146-731-234	Sequence 234, App
	24	42.6	4.7	1160	6	US-10-140-472-234	Sequence 234, App
	25	42.6	4.7	1160	6	US-10-141-761-234	Sequence 234, App
	26	42.6	4.7	1160	6	US-10-142-885-234	Sequence 234, App
	27	42.6	4.7	1160	6	US-10-158-790-234	Sequence 234, App
	28	42.6	4.7	1160	6	US-10-137-871-234	Sequence 234, App
	29	42.6	4.7	1160	6	US-10-140-923-234	Sequence 234, App
	30	42.6	4.7	1160	6	US-10-141-756-234	Sequence 234, App
	31	42.6	4.7	1160	6	US-10-141-759-234	Sequence 234, App
	32	42.6	4.7	1160	6	US-10-140-805-234	Sequence 234, App
	33	42.6	4.7	1160	6	US-10-140-864-234	Sequence 234, App
	34	40.2	4.4	849	7	US-10-282-122A-11182	Sequence 11182, A
c	35	40	4.4	680	8	US-10-653-047-1226	Sequence 1226, Ap
c	36	38.6	4.2	438	8	US-10-674-124A-11007	Sequence 11007, A
c	37	38.4	4.2	4083	7	US-10-437-963-83237	Sequence 83237, A
	38	38	4.2	693	7	US-10-282-122A-13506	Sequence 13506, A
	39	37.8	4.1	726	6	US-10-369-493-42851	Sequence 42851, A
c	40	37.8	4.1	745	7	US-10-437-963-83233	Sequence 83233, A
c	41	37.6	4.1	529	8	US-10-425-115-115884	Sequence 115884,
	42	37.4	4.1	2042	7	US-10-437-963-1603	Sequence 1603, Ap
	43	37	4.1	696	7	US-10-282-122A-13625	Sequence 13625, A
c	44	36.6	4.0	594	5	US-10-123-155-10	Sequence 10, Appl
c	45	36.6	4.0	594	6	US-10-146-731-10	Sequence 10, Appl

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2006, 22:58:26 ; Search time 3731 Seconds
(without alignments)
11436.564 Million cell updates/sec

Title: US-10-694-779-9
Perfect score: 912
Sequence: 1 atgtgacgacggagtcctag.....cacttcacgcagactcgcac 912

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hlc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%		Query			Description
Result	No.	Score	Match	Length	DB	ID	
c	1	81.6	8.9	426	2	BI062358	BI062358 IL3-UT011
	2	47.6	5.2	1069	8	DR738787	DR738787 FGAS08400
	3	46.6	5.1	839	10	AG882978	AG882978 Oryza sat
	4	46	5.0	475	8	DN180328	DN180328 HO27G01S
	5	46	5.0	612	8	DN181015	DN181015 HO25H19S
	6	46	5.0	1000	1	AU252302	AU252302 AU252302

7	46	5.0	1316	1	AU252292	AU252292 AU252292
8	45.6	5.0	654	10	CW138494	CW138494 104_528_1
9	44.6	4.9	405	8	DN180329	DN180329 HO27G02S
10	44.6	4.9	835	8	CV776873	CV776873 FGAS07127
11	44.6	4.9	1146	7	CK166509	CK166509 FGAS05066
12	43.6	4.8	687	10	AG946800	AG946800 Drosophil
13	43	4.7	662	3	BJ281216	BJ281216 BJ281216
14	43	4.7	695	6	CD882228	CD882228 Fl.105M13
15	43	4.7	857	8	CV763444	CV763444 FGAS05783
16	43	4.7	969	8	CV770252	CV770252 FGAS06464
17	43	4.7	1105	8	DR739375	DR739375 FGAS08459
18	43	4.7	1169	7	CK162000	CK162000 FGAS01458
19	42.6	4.7	257	1	AL828709	AL828709 AL828709
20	42.6	4.7	443	6	CD461012	CD461012 Fg09_03g1
c 21	42	4.6	501	6	CD116784	CD116784 ME1-0043T
c 22	42	4.6	593	10	AG937790	AG937790 Drosophil
c 23	41.4	4.5	577	5	BU060496	BU060496 Fgr-C_1_D
24	41.4	4.5	581	5	BU060034	BU060034 Fgr-C_0_J
c 25	41.4	4.5	609	5	BU063571	BU063571 Fgr_3_E16
c 26	41.4	4.5	635	5	BU065578	BU065578 Fgr_7_P05
27	41.4	4.5	661	5	BU062199	BU062199 Fgr_1_H15
28	41.4	4.5	669	5	BU060497	BU060497 Fgr-C_1_D
29	41.4	4.5	670	5	BU063126	BU063126 Fgr_2_L07
30	41.4	4.5	704	5	BU061251	BU061251 FgrN_5_M1
31	41.4	4.5	712	5	BU063572	BU063572 Fgr_3_E16
32	40.4	4.4	823	7	CK200509	CK200509 FGAS00902
33	40.2	4.4	997	10	CNS005TE	AL060767 Drosophil
c 34	39.8	4.4	488	5	BU063125	BU063125 Fgr_2_L07
c 35	39.8	4.4	494	5	BU060033	BU060033 Fgr-C_0_J
36	39	4.3	568	5	BQ838054	BQ838054 WHE2906_A
37	39	4.3	636	3	BI954020	BI954020 HVSME001
38	38.8	4.3	530	3	BJ244886	BJ244886 BJ244886
39	38.8	4.3	562	3	BI774730	BI774730 466936 MA
c 40	38.8	4.3	741	7	CK358958	CK358958 AGENCOURT
41	38.8	4.3	861	7	CK203625	CK203625 FGAS01215
c 42	38.4	4.2	458	7	CF964603	CF964603 12818rsic
c 43	38.4	4.2	573	10	CZ632396	CZ632396 OM__Ba017
44	38.4	4.2	779	7	CO387234	CO387234 AGENCOURT
c 45	38.2	4.2	470	5	BU062198	BU062198 Fgr_1_H15

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OM nucleic - nucleic search, using sw model

Run on: March 17, 2006, 09:15:55 ; Search time 4968 Seconds
 (without alignments)
 12744.481 Million cell updates/sec

Title: US-10-694-779-21
 Perfect score: 9500
 Sequence: 1 acctcgtatgggcagtaatt.....acgggcaacgcgtccgcggg 9500

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_21:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	9500	100.0	9500	6	ABL54671	Abl54671 Corynebac
2	4227.4	44.5	349980	5	AAH68528	Aah68528 C glutami
3	1749.2	18.4	110000	4	AAI99682_14	Continuation (15 o

	4	1749.2	18.4	110000	4	AAI99683_14	Continuation (15 o
c	5	1732.4	18.2	36241	10	ADB74385	Adb74385 Mycobacte
c	6	1667.2	17.5	349980	6	ABQ81844	Abq81844 Bifidobac
	7	1638	17.2	1638	6	ABL54663	Abl54663 Corynebac
c	8	1474.2	15.5	20798	4	AAS59620	Aas59620 Propionib
c	9	1474.2	15.5	20798	8	ACF64549	Acf64549 Propionib
	10	1443	15.2	1443	6	ABL54665	Abl54665 Corynebac
	11	1170.8	12.3	1572	4	AAF71740	Aaf71740 Corynebac
	12	1159	12.2	1764	4	AAF71739	Aaf71739 Corynebac
	13	1158.6	12.2	1674	5	AAH66305	Aah66305 C glutami
	14	1137.2	12.0	1659	8	ACA29625	Aca29625 Prokaryot
	15	1097.8	11.6	1452	2	AAT03954	Aat03954 Brevibact
	16	1092.6	11.5	1449	5	AAH66307	Aah66307 C glutami
	17	981	10.3	981	6	ABL54664	Abl54664 Corynebac
	18	912	9.6	912	6	ABL54659	Abl54659 Corynebac
	19	853.8	9.0	8008	2	AAZ32024	Aaz32024 Human MET
	20	853.8	9.0	8009	5	AAC90081	Aac90081 X99599 cD
	21	849.8	8.9	110000	6	ABQ67196_5	Continuation (6 of
c	22	849.8	8.9	110000	6	ABQ69245_26	Continuation (27 o
c	23	833.8	8.8	110000	6	ABA03041_25	Continuation (26 o
c	24	833.8	8.8	110000	6	ABA03041_26	Continuation (27 o
	25	813	8.6	813	6	ABL54662	Abl54662 Corynebac
	26	805	8.5	1662	8	ACA38144	Aca38144 Prokaryot
	27	799.4	8.4	1920	5	AAS03789	Aas03789 Mycobacte
	28	780.4	8.2	10399	2	AAV52293	Aav52293 Streptoco
c	29	780.4	8.2	110000	10	ABS56454_13	Continuation (14 o
	30	772	8.1	1521	13	ADS56270	Ads56270 Bacterial
c	31	769.2	8.1	46593	3	AAA81456	Aaa81456 N. mening
c	32	769.2	8.1	110000	3	AAA81489_5	Continuation (6 of
c	33	769.2	8.1	349980	3	AAF21612	Aaf21612 Neisseria
	34	765.2	8.1	1647	8	ACA38774	Aca38774 Prokaryot
	35	765.2	8.1	1650	8	ACA40479	Aca40479 Prokaryot
	36	758.6	8.0	4815	2	AAV29571	Aav29571 L. lactis
	37	757.4	8.0	1413	13	ADS56268	Ads56268 Bacterial
	38	751.4	7.9	7750	2	AAX13153	Aax13153 Enterococ
	39	751.4	7.9	7750	6	ABS98948	Abs98948 Enterococ
	40	751	7.9	110000	10	ADF77343_10	Continuation (11 o
	41	734.2	7.7	71979	13	ADV87736	Adv87736 Streptoco
	42	734.2	7.7	71979	13	ADV78989	Adv78989 Streptoco
	43	734.2	7.7	110000	6	ABN71527_08	Continuation (9 of
	44	734.2	7.7	110000	13	ADV81204_09	Continuation (10 o
	45	732.8	7.7	1677	8	ACA39764	Aca39764 Prokaryot

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OM nucleic - nucleic search, using sw model

Run on: March 17, 2006, 19:30:20 ; Search time 4417 Seconds
(without alignments)
17785.622 Million cell updates/sec

Title: US-10-694-779-21
Perfect score: 9500
Sequence: 1 acctcgtatgggcagtaatt.....acgggcaacgcgtccgcggg 9500

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	9500	100.0	9500	3	US-09-901-884-21	Sequence 21, Appl
2	9500	100.0	9500	8	US-10-694-779-21	Sequence 21, Appl
3	4227.4	44.5	3309400	3	US-09-738-626-1	Sequence 1, Appli
c 4	1667.2	17.5	2256646	7	US-10-470-565-1	Sequence 1, Appli
5	1665.2	17.5	125746	6	US-10-156-761-15102	Sequence 15102, A
c 6	1665.2	17.5	9025608	6	US-10-156-761-1	Sequence 1, Appli
7	1638	17.2	1638	3	US-09-901-884-13	Sequence 13, Appl

	8	1638	17.2	1638	8	US-10-694-779-13	Sequence 13, Appl
	9	1443	15.2	1443	3	US-09-901-884-15	Sequence 15, Appl
	10	1443	15.2	1443	8	US-10-694-779-15	Sequence 15, Appl
	11	1170.8	12.3	1572	8	US-10-781-014-761	Sequence 761, App
	12	1159	12.2	1764	8	US-10-781-014-759	Sequence 759, App
	13	1158.6	12.2	1674	3	US-09-738-626-1340	Sequence 1340, Ap
	14	1137.2	12.0	1659	7	US-10-282-122A-17495	Sequence 17495, A
	15	1092.6	11.5	1449	3	US-09-738-626-1342	Sequence 1342, Ap
	16	981	10.3	981	3	US-09-901-884-14	Sequence 14, Appl
	17	981	10.3	981	8	US-10-694-779-14	Sequence 14, Appl
	18	912	9.6	912	3	US-09-901-884-9	Sequence 9, Appli
	19	912	9.6	912	8	US-10-694-779-9	Sequence 9, Appli
	20	853.8	9.0	8009	3	US-09-373-658-34	Sequence 34, Appl
	21	853.8	9.0	8009	3	US-09-989-687-34	Sequence 34, Appl
	22	849.8	8.9	684707	7	US-10-398-221-9	Sequence 9, Appli
c	23	849.8	8.9	3011208	7	US-10-398-221-2058	Sequence 2058, Ap
	24	813	8.6	813	3	US-09-901-884-12	Sequence 12, Appl
	25	813	8.6	813	8	US-10-694-779-12	Sequence 12, Appl
	26	805	8.5	1662	7	US-10-282-122A-26014	Sequence 26014, A
	27	780.4	8.2	10399	2	US-08-961-527-160	Sequence 160, App
	28	780.4	8.2	10399	7	US-10-158-844-160	Sequence 160, App
c	29	780.4	8.2	2162598	8	US-10-472-928-4979	Sequence 4979, Ap
	30	772	8.1	1521	6	US-10-369-493-31944	Sequence 31944, A
c	31	769.2	8.1	46594	9	US-10-915-740A-4	Sequence 4, Appli
c	32	769.2	8.1	2242716	9	US-10-915-740A-1068	Sequence 1068, Ap
	33	765.2	8.1	1647	7	US-10-282-122A-26644	Sequence 26644, A
	34	765.2	8.1	1650	7	US-10-282-122A-28349	Sequence 28349, A
	35	758.6	8.0	4815	6	US-10-310-630-1	Sequence 1, Appli
	36	757.4	8.0	1413	6	US-10-369-493-31942	Sequence 31942, A
	37	751.4	7.9	7750	3	US-09-070-927A-216	Sequence 216, App
	38	739.2	7.8	1587	6	US-10-156-761-2870	Sequence 2870, Ap
	39	732.8	7.7	1677	7	US-10-282-122A-27634	Sequence 27634, A
c	40	720	7.6	2731748	7	US-10-297-465A-1	Sequence 1, Appli
	41	708.8	7.5	1434	6	US-10-156-761-2868	Sequence 2868, Ap
	42	703.8	7.4	6901	8	US-10-857-625-130	Sequence 130, App
	43	629	6.6	778	8	US-10-781-014-763	Sequence 763, App
	44	603.8	6.4	1515	6	US-10-369-493-35121	Sequence 35121, A
	45	594.6	6.3	1527	6	US-10-369-493-34379	Sequence 34379, A

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OM nucleic - nucleic search, using sw model

Run on: March 17, 2006, 12:34:04 ; Search time 22063 Seconds
(without alignments)
20145.823 Million cell updates/sec

Title: US-10-694-779-21
Perfect score: 9500
Sequence: 1 acctcgtatgggcagtaatt.....acgggcaacgcgtccgcggg 9500

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query				ID	Description
		Match	Length	DB			
1	538.6	5.7	1613	4	CNS0EQFJ		CR636937 Tetraodon
2	529.6	5.6	2076	4	AY849656		AY849656 Magnaport
3	529.4	5.6	2196	4	AK043976		AK043976 Mus muscu
4	529.4	5.6	2197	4	AK076572		AK076572 Mus muscu
5	527.2	5.5	1821	4	CNS0EPRY		CR636088 Tetraodon
6	526.2	5.5	1847	4	BC020417		BC020417 Mus muscu

7	513	5.4	1910	4	CR861028	CR861028	Pongo pyg
8	510.8	5.4	1845	7	CN210866	CN210866	WLA073D01
9	510.8	5.4	1864	7	CN210865	CN210865	RJA108H07
10	510.4	5.4	1844	4	BC042694	BC042694	Homo sapi
11	509.8	5.4	1675	4	CNS0GQK6	CR730449	Tetraodon
12	508.8	5.4	1767	4	CR604755	CR604755	full-leng
13	508.8	5.4	1768	4	CR591462	CR591462	full-leng
14	508.8	5.4	1769	4	CR617088	CR617088	full-leng
15	508.8	5.4	1793	4	CR625409	CR625409	full-leng
16	508.8	5.4	1803	4	CR607960	CR607960	full-leng
17	508.8	5.4	1804	4	CR611390	CR611390	full-leng
18	508.8	5.4	1806	4	CR593595	CR593595	full-leng
19	508.8	5.4	1809	4	CR590601	CR590601	full-leng
20	508.8	5.4	1811	4	CR609973	CR609973	full-leng
21	508.8	5.4	1812	4	CR613857	CR613857	full-leng
22	508.8	5.4	1814	4	CR604007	CR604007	full-leng
23	508.8	5.4	1814	4	CR617331	CR617331	full-leng
24	508.8	5.4	1815	4	CR591138	CR591138	full-leng
25	508.8	5.4	1815	4	CR594700	CR594700	full-leng
26	508.8	5.4	1816	4	CR608051	CR608051	full-leng
27	508.8	5.4	1823	4	CR609069	CR609069	full-leng
28	508.8	5.4	1825	4	CR610155	CR610155	full-leng
29	508.8	5.4	1826	4	CR590562	CR590562	full-leng
30	508.8	5.4	1827	4	CR609904	CR609904	full-leng
31	508.8	5.4	1827	4	CR617880	CR617880	full-leng
32	508.8	5.4	1827	4	CR626813	CR626813	full-leng
33	508.8	5.4	1829	4	CR599938	CR599938	full-leng
34	508.8	5.4	1829	4	CR601229	CR601229	full-leng
35	508.8	5.4	1829	4	CR617650	CR617650	full-leng
36	508.8	5.4	1829	4	CR622375	CR622375	full-leng
37	508.8	5.4	1834	4	CR597477	CR597477	full-leng
38	508.8	5.4	1837	4	CR626480	CR626480	full-leng
39	508.8	5.4	1839	4	CR604077	CR604077	full-leng
40	508.8	5.4	1842	4	CR597489	CR597489	full-leng
41	508.8	5.4	1861	4	BC028335	BC028335	Homo sapi
42	508.2	5.3	1681	4	CNS0FGAK	CR670454	Tetraodon
43	507.6	5.3	1559	4	CR625663	CR625663	full-leng
44	505.2	5.3	1682	4	CNS0FYTV	CR694503	Tetraodon
45	500.4	5.3	1672	4	CNS0FNQU	CR680138	Tetraodon

OM nucleic - nucleic search, using sw model

Run on: March 15, 2006, 22:49:07 ; Search time 4713 Seconds
(without alignments)
10999.624 Million cell updates/sec

Title: US-10-694-779-9
Perfect score: 912
Sequence: 1 atgtgcgacggagtcctag.....cacttcacgcagactcgac 912

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	912	100.0	912	6	BD133255	BD133255 FOF1-ATPa
2	912	100.0	9500	6	BD133267	BD133267 FOF1-ATPa
3	504.2	55.3	8394	1	AB046112	AB046112 Corynebac
4	504.2	55.3	110000	1	BA000036_12	Continuation (13 o
5	504.2	55.3	349459	1	BX927151	BX927151 Corynebac
6	504.2	55.3	349980	6	AX127147	AX127147 Sequence
7	502.6	55.1	8001	1	AB048368	AB048368 Brevibact
8	499.2	54.7	110000	1	BA000035_13	Continuation (14 o
9	488.2	53.5	933	6	AX065629	AX065629 Sequence
10	456.2	50.0	862	6	AX065631	AX065631 Sequence
11	454	49.8	347625	1	BX248356	BX248356 Corynebac
12	443.6	48.6	810	6	BD163537	BD163537 Novel pol
13	443.6	48.6	810	6	AX121420	AX121420 Sequence
c 14	435	47.7	110000	1	CR931997_15	Continuation (16 o
15	288.6	31.6	110000	1	AP006618_11	Continuation (12 o
16	190.8	20.9	110000	1	AE016822_06	Continuation (7 of
17	190.8	20.9	110000	1	AE016822_07	Continuation (8 of

	18	134.6	14.8	299050	1	BX251411	BX251411 Tropherym
c	19	134.6	14.8	302529	1	AE016851	AE016851 Tropherym
	20	134.2	14.7	8560	1	SLATPSYNA	Z22606 S.lividans
	21	134.2	14.7	300100	1	SCO939123	AL939123 Streptomy
	22	127.4	14.0	7760	1	AY702091	AY702091 Nonomurae
c	23	120.6	13.2	8323	1	AY488175	AY488175 Bifidobac
c	24	119.4	13.1	110000	1	BA000030_35	Continuation (36 o
c	25	118.8	13.0	110000	1	AE014295_12	Continuation (13 o
c	26	118.8	13.0	349980	6	AX492782	AX492782 Sequence
c	27	118.8	13.0	349980	6	AX553949	AX553949 Sequence
c	28	102	11.2	110000	1	CP000088_28	Continuation (29 o
	29	95	10.4	8358	1	AY488174	AY488174 Bifidobac
	30	71.2	7.8	110000	1	BA000012_61	Continuation (62 o
	31	60	6.6	7218	6	I66494	I66494 Sequence 14
	32	59.2	6.5	2220	1	AF054609	AF054609 Brucella
c	33	59.2	6.5	12028	1	AE009590	AE009590 Brucella
	34	59.2	6.5	110000	1	AE014291_03	Continuation (4 of
	35	59.2	6.5	110000	1	AE017223_04	Continuation (5 of
c	36	55.6	6.1	11283	1	AE005710	AE005710 Caulobact
	37	51.6	5.7	31495	1	BJU33883	U33883 Bradyrhizob
c	38	51.6	5.7	110000	1	BA000040_12	Continuation (13 o
c	39	51.6	5.7	110000	1	BA000040_13	Continuation (14 o
	40	50.8	5.6	843	6	AR621598	AR621598 Sequence
c	41	50.8	5.6	1394	6	AR618970	AR618970 Sequence
	42	48.8	5.4	4364	6	CQ363872	CQ363872 Sequence
c	43	48.8	5.4	110000	1	AE017283_13	Continuation (14 o
	44	48.4	5.3	12152	1	AE009040	AE009040 Agrobacte
	45	48.4	5.3	12164	1	AE008006	AE008006 Agrobacte

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2006, 05:51:17 ; Search time 370 Seconds
(without alignments)
4381.449 Million cell updates/sec

Title: US-10-694-779-9
Perfect score: 912
Sequence: 1 atgtgcgacggagtccgtag.....cacttcacgcagactcgcac 912

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	60	6.6	7218	2	US-08-232-463-14	Sequence 14, Appl
	2	50.8	5.6	843	3	US-09-902-540-2999	Sequence 2999, Ap
c	3	50.8	5.6	1394	3	US-09-902-540-365	Sequence 365, App
	4	44.6	4.9	1703	3	US-09-370-253-9	Sequence 9, Appli
c	5	40	4.4	680	3	US-09-533-559-1226	Sequence 1226, Ap
c	6	39	4.3	1581	3	US-09-936-145-15	Sequence 15, Appl
	7	37.8	4.1	702	3	US-09-902-540-7194	Sequence 7194, Ap
c	8	37.8	4.1	6430	3	US-09-902-540-669	Sequence 669, App
	9	37	4.1	663	3	US-09-489-039A-353	Sequence 353, App

	10	36.6	4.0	1865	3	US-09-370-253-5	Sequence 5, Appli
	11	35.6	3.9	1656	3	US-09-902-540-6804	Sequence 6804, Ap
c	12	35.6	3.9	3487	3	US-09-902-540-561	Sequence 561, App
c	13	35	3.8	1083	3	US-09-252-991A-1074	Sequence 1074, Ap
	14	35	3.8	1372	3	US-09-270-767-13796	Sequence 13796, A
	15	35	3.8	1692	3	US-09-252-991A-978	Sequence 978, App
	16	35	3.8	1836	3	US-09-252-991A-1026	Sequence 1026, Ap
	17	34.8	3.8	747	3	US-09-252-991A-14108	Sequence 14108, A
	18	34.8	3.8	1035	3	US-09-252-991A-14017	Sequence 14017, A
c	19	34.8	3.8	1365	3	US-09-252-991A-14122	Sequence 14122, A
	20	34.8	3.8	1574	3	US-09-902-540-2466	Sequence 2466, Ap
	21	34.8	3.8	2019	3	US-09-063-950-3	Sequence 3, Appli
	22	34.8	3.8	2555	3	US-09-866-028-68	Sequence 68, Appl
	23	34.8	3.8	2555	3	US-09-944-457-68	Sequence 68, Appl
	24	34.8	3.8	2555	3	US-09-945-584-68	Sequence 68, Appl
	25	34.8	3.8	2555	3	US-09-944-944-68	Sequence 68, Appl
	26	34.8	3.8	2555	3	US-09-945-587-68	Sequence 68, Appl
	27	34.8	3.8	2768	3	US-09-991-181-51	Sequence 51, Appl
	28	34.8	3.8	2768	3	US-09-990-444-51	Sequence 51, Appl
	29	34.8	3.8	2768	3	US-09-997-333-51	Sequence 51, Appl
	30	34.8	3.8	2768	3	US-09-992-598-51	Sequence 51, Appl
	31	34.8	3.8	2852	3	US-09-063-950-1	Sequence 1, Appli
c	32	34.8	3.8	14077	3	US-09-902-540-1109	Sequence 1109, Ap
	33	34.4	3.8	505	3	US-09-621-976-15639	Sequence 15639, A
	34	34.4	3.8	219964	3	US-09-949-016-15086	Sequence 15086, A
	35	34	3.7	1080	3	US-09-875-076-27	Sequence 27, Appl
	36	34	3.7	3626	3	US-09-620-312D-93	Sequence 93, Appl
c	37	33.8	3.7	14807	3	US-09-902-540-1085	Sequence 1085, Ap
c	38	33.6	3.7	525	3	US-09-252-991A-9910	Sequence 9910, Ap
c	39	33.6	3.7	723	3	US-09-252-991A-10004	Sequence 10004, A
	40	33.6	3.7	744	3	US-09-252-991A-10165	Sequence 10165, A
	41	33.6	3.7	870	3	US-09-252-991A-6993	Sequence 6993, Ap
	42	33.6	3.7	1191	3	US-09-252-991A-7232	Sequence 7232, Ap
c	43	33.6	3.7	1218	3	US-09-252-991A-7465	Sequence 7465, Ap
	44	33.6	3.7	1248	3	US-09-252-991A-7180	Sequence 7180, Ap
	45	33.6	3.7	1254	3	US-09-252-991A-10100	Sequence 10100, A

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OM nucleic - nucleic search, using sw model

Run on: March 16, 2006, 15:33:28 ; Search time 434 Seconds
 (without alignments)
 4899.806 Million cell updates/sec

Title: US-10-694-779-9
 Perfect score: 912
 Sequence: 1 atgtgacgacggagtcctag.....cacttcacgcagactcgcac 912

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications_NA_New:*
 1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
 4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
 5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
 6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
 7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
 8: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
 10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
 11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
 12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB	ID	Description
	Score	Match Length			
1	36.4	4.0	1536	9 US-11-096-568A-22147	Sequence 22147, A
2	36.4	4.0	1791	9 US-11-096-568A-18969	Sequence 18969, A
3	36.2	4.0	1792	9 US-11-096-568A-23390	Sequence 23390, A
4	35.8	3.9	1400	12 US-11-136-527-7196	Sequence 7196, Ap

	5	35.8	3.9	1745	12	US-11-136-527-3100	Sequence 3100, Ap
c	6	35.2	3.9	624	8	US-10-467-657-5841	Sequence 5841, Ap
c	7	35.2	3.9	624	8	US-10-467-657-7481	Sequence 7481, Ap
	8	34.8	3.8	2768	7	US-10-063-703-15	Sequence 15, Appl
	9	34.8	3.8	2768	9	US-11-103-195-15	Sequence 15, Appl
	10	34.8	3.8	2768	12	US-11-102-240-15	Sequence 15, Appl
c	11	34.2	3.8	599	12	US-11-128-061-3933	Sequence 3933, Ap
c	12	34.2	3.8	599	12	US-11-128-049-3933	Sequence 3933, Ap
c	13	34.2	3.8	680	12	US-11-128-061-291	Sequence 291, App
c	14	34.2	3.8	680	12	US-11-128-049-291	Sequence 291, App
	15	34	3.7	635	6	US-09-925-065A-37710	Sequence 37710, A
c	16	33.8	3.7	1146	7	US-10-932-182A-2328	Sequence 2328, Ap
c	17	33.8	3.7	1146	7	US-10-932-182A-2328	Sequence 2328, Ap
	18	33.6	3.7	818	11	US-11-082-389-189	Sequence 189, App
	19	33.6	3.7	415117	8	US-10-995-561-13274	Sequence 13274, A
c	20	33.2	3.6	1295	9	US-11-096-568A-22518	Sequence 22518, A
	21	33	3.6	52192	8	US-10-995-561-13231	Sequence 13231, A
c	22	32.8	3.6	2877	7	US-10-932-182A-2501	Sequence 2501, Ap
c	23	32.8	3.6	2877	7	US-10-932-182A-2501	Sequence 2501, Ap
	24	32.6	3.6	1584	7	US-10-932-182A-5584	Sequence 5584, Ap
	25	32.6	3.6	1584	7	US-10-932-182A-5584	Sequence 5584, Ap
	26	32.4	3.6	1691	9	US-11-096-568A-18453	Sequence 18453, A
c	27	32.4	3.6	2601	11	US-11-077-550-79	Sequence 79, Appl
c	28	32.4	3.6	2664	11	US-11-077-550-111	Sequence 111, App
c	29	32.4	3.6	4665	12	US-11-136-527-3309	Sequence 3309, Ap
	30	32.2	3.5	630	6	US-09-925-065A-895235	Sequence 895235,
	31	32.2	3.5	630	6	US-09-925-065A-916450	Sequence 916450,
c	32	32	3.5	310	6	US-09-925-065A-496311	Sequence 496311,
c	33	32	3.5	2609	9	US-11-072-512-1365	Sequence 1365, Ap
c	34	31.8	3.5	507	12	US-11-052-554A-699	Sequence 699, App
	35	31.8	3.5	622	12	US-11-136-527-3624	Sequence 3624, Ap
c	36	31.8	3.5	622	12	US-11-136-527-7720	Sequence 7720, Ap
c	37	31.8	3.5	4026	12	US-11-149-003-23	Sequence 23, Appl
c	38	31.8	3.5	4431	12	US-11-149-003-7	Sequence 7, Appli
c	39	31.8	3.5	4536	12	US-11-149-003-9	Sequence 9, Appli
c	40	31.8	3.5	4779	12	US-11-149-003-3	Sequence 3, Appli
c	41	31.8	3.5	4884	12	US-11-149-003-1	Sequence 1, Appli
c	42	31.8	3.5	5776	12	US-11-149-003-25	Sequence 25, Appl
	43	31.8	3.5	88421	12	US-11-205-109-1	Sequence 1, Appli
	44	31.8	3.5	172543	12	US-11-121-086-6	Sequence 6, Appli
c	45	31.6	3.5	576	6	US-09-925-065A-310255	Sequence 310255,